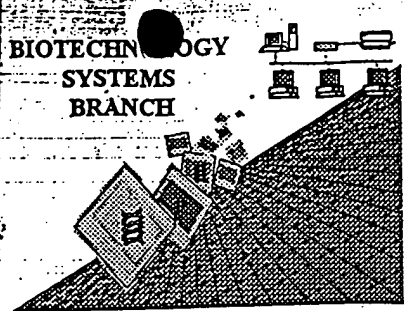


PIC 49179
(1965)

RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



0566

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/618,424

Source: OIFE

Date Processed by STIC: 7/28/2000

Sequence Listing

Dike, Bronstein, Roberts & Cushman, LL

130 Water St. Boston, MA 02108

Date Rec'd, 8/25/00

Docketed For Sep. 22, 2000 - Feb. 22, 2001

By KRD

Approved _____

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

New Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/618,424

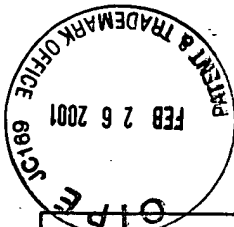
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE



- | | | |
|----|----------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 2 | Wrapped Nucleics | The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping". |
| 2 | Wrapped Aminos | The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping". |
| 3 | Incorrect Line Length | The rules require that a line not exceed 72 characters in length. This includes spaces. |
| 4 | Misaligned Amino Acid Numbering | The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers. |
| 5 | Non-ASCII | This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed. |
| 6 | Variable Length | Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing. |
| 7 | PatentIn ver. 2.0 "bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences. |
| 8 | Skipped Sequences (OLD RULES) | Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xl) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s). |
| 9 | Skipped Sequences (NEW RULES) | Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000 |
| 10 | Use of n's or Xaa's (NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. |
| 11 | Use of <213>Organism (NEW RULES) | Sequence(s) ____ are missing this mandatory field or its response. |
| 12 | Use of <220>Feature (NEW RULES) | Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules) |
| 13 | PatentIn ver. 2.0 "bug" | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk. |

PAGE: 1



RAW SEQUENCE LISTING
PATENT APPLICATION US/09/618,424

DATE: 07/28/2000
TIME: 13:43:18

Input Set: I618424.RAW

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

Does Not Comply

Corrected Diskette Needed

E--> 1 <110> *insert the mandatory numeric identifiers and their responses?*
E--> 2 <120>
W--> OK 3 <130>
4 <140> US/09/618,424
5 <141> 2000-07-18
6 <160> 20
7 <170> PatentIn Ver. 2.0

*All Item 13 on Error Summary
sheet for possible
explanation of missing
items*

ERRORED SEQUENCES FOLLOW

8 <210> 20
9 <211> 21
10 <212> PRT
11 <213> Artificial Sequence
12 <220>
13 <223> Description of Artificial Sequence: Artificial
14 Sequence
15 <400> 20
16 Ser Gly Arg Gly Lys Gly Gly Lys Gly Leu Gly Lys Gly Gly Ala Lys
17 1 5 10 15
18 Arg His Arg Lys Cys
19 20
20 1
21 1

*inserted response - give source of genetic
material. See circled
portion of Item 12 on
Error Summary
sheet.*

delete

HAPT "SYNTHETIC"

EXAMINER McCaa:
(DIRECT LINE)

EXAMINER:

TERRY McCaa
308-1234
305-3298

(703) 605-1207

Input Set: I618424.RAW

Line ? Error/Warning

Original Text

-
- 1 E Response to "Applicant" Name is Missing
 - 2 E Response to "Title of Invention" Missing
 - 3 W Response to "File Reference" is Missing
 - 21 E Invalid/Missing Amino Acid Numbering 1

